



SEQUENCE LISTING

SEQ ID NO: 1 is mouse TECK nucleotide sequence.
SEQ ID NO: 2 is mouse TECK amino acid sequence.
SEQ ID NO: 3 is human TECK nucleotide sequence.
SEQ ID NO: 4 is human TECK amino acid sequence.
SEQ ID NO: 5 is human MIP-3 α nucleotide sequence.
SEQ ID NO: 6 is human MIP-3 α amino acid sequence.
SEQ ID NO: 7 is human MIP-3 β nucleotide sequence.
SEQ ID NO: 8 is human MIP-3 β amino acid sequence.
SEQ ID NO: 9 is human DC CR nucleotide sequence.
SEQ ID NO: 10 is human DC CR amino acid sequence.
SEQ ID NO: 11 is human M/DC CR nucleotide sequence.
SEQ ID NO: 12 is human M/DC CR amino acid sequence.
SEQ ID NO: 13 is human CCKR1 amino acid sequence.
SEQ ID NO: 14 is human CCKR2 amino acid sequence.
SEQ ID NO: 15 is human CCKR3 amino acid sequence.
SEQ ID NO: 16 is human CCKR4 amino acid sequence.
SEQ ID NO: 17 is HPRT sense primer.
SEQ ID NO: 18 is HPRT antisense primer.
SEQ ID NO: 19 is FLAG epitope tag sequence.

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS

(iii) NUMBER OF SEQUENCES: 19

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/887,977
(B) FILING DATE: 03-JUL-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/021,644
(B) FILING DATE: 05-JUL-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/028,329

(B) FILING DATE: 11-OCT-1996

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1034 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 94..525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

B' cont.

AGGCTACAAG CAGGCACCAG CTCTCAGGAC CAGAAAGGCA TTGGTGGCCC CCTTAAACCT	60
TCAGGTATCT GGAGAGGAGA TCTAACCTTC ACT ATG AAA CTG TGG CTT TTT GCC	114
Met Lys Leu Trp Leu Phe Ala	
1 5	
TGC CTG GTT GCC TGT TTT GTT GGG GCC TGG ATG CCG GTT GTC CAT GCC	162
Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala	
10 15 20	
CAA GGT GCC TTT GAA GAC TGC TGC CTG GGT TAC CAG CAC AGG ATC AAA	210
Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys	
25 30 35	
TGG AAT GTT CTC CGG CAT GCT AGG AAT TAT CAC CAG CAG GAA GTG AGT	258
Trp Asn Val Leu Arg His Ala Arg Asn Tyr His Gln Gln Glu Val Ser	
40 45 50 55	
GGA AGC TGC AAC CTA CGT GCT GTG AGA TTC TAC TTC CGC CAG AAA GTA	306
Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val	
60 65 70	
GTG TGT GGG AAT CCA GAG GAC ATG AAT GTG AAG AGG GCG ATA AGA ATC	354
Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile	
75 80 85	

[illegible]

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

50	Met	Lys	Leu	Trp	Leu	Phe	Ala	Cys	Leu	Val	Ala	Cys	Phe	Val	Gly	Ala
	1				5					10					15	
	Trp	Met	Pro	Val	Val	His	Ala	Gln	Gly	Ala	Phe	Glu	Asp	Cys	Cys	Leu
				20					25					30		
55	Gly	Tyr	Gln	His	Arg	Ile	Lys	Trp	Asn	Val	Leu	Arg	His	Ala	Arg	Asn
			35					40					45			
	Tyr	His	Gln	Gln	Glu	Val	Ser	Gly	Ser	Cys	Asn	Leu	Arg	Ala	Val	Arg
	50						55					60				

Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn
 65 70 75 80
 5 Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His
 85 90 95
 Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His
 100 105 110
 10 Met Lys Ser Lys Val Glu Asn Pro Asn Ser Thr Ser Val Arg Ser Ala
 115 120 125
 Thr Leu Gly His Pro Arg Met Val Met Met Pro Arg Lys Thr Asn Asn
 15 130 135 140

(2) INFORMATION FOR SEQ ID NO:3:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1012 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 117..566

35 (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 186..566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40 TCGACCCACG CGTCCGCTTG GCCTACAGCC CGGCGGGCAT CAGCTCCCTT GACCCAGTGG 60
 ATATCGGTGG CCCCGTTATT CGTCCAGGTG CCCAGGGAGG AGGACCCGCC TGCAGC 116
 ATG AAC CTG TGG CTC CTG GCC TGC CTG GTG GCC GGC TTC CTG GGA GCC 164
 45 Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
 -23 -20 -15 -10
 TGG GCC CCC GCT GTC CAC ACC CAA GGT GTC TTT GAG GAC TGC TGC CTG 212
 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
 50 -5 1 5
 GCC TAC CAC TAC CCC ATT GGG TGG GCT GTG CTC CGG CGC GCC TGG ACT 260
 Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
 10 15 20 25
 55 TAC CGG ATC CAG GAG GTG AGC GGG AGC TGC AAT CTG CCT GCT GCG ATA 308
 Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
 30 35 40

5	TTC TAC CTC CCC AAG AGA CAC AGG AAG GTG TGT GGG AAC CCC AAA AGC	356
	Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser	
	45 50 55	
	AGG GAG GTG CAG AGA GCC ATG AAG CTC CTG GAT GCT CGA AAT AAG GTT	404
	Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val	
10	60 65 70	
	TTT GCA AAG CTC CAC CAC AAC ATG CAG ACC TTC CAA GCA GGC CCT CAT	452
	Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His	
	75 80 85	
	GCT GTA AAG AAG TTG AGT TCT GGA AAC TCC AAG TTA TCA TCA TCC AAG	500
15	Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys	
	90 95 100 105	
	TTT AGC AAT CCC ATC AGC AGC AGC AAG AGG AAT GTC TCC CTC CTG ATA	548
	Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile	
	110 115 120	
20	TCA GCT AAT TCA GGA CTG TGAGCCGGCT CATTTCTGGG CTCCATCGGC	596
	Ser Ala Asn Ser Gly Leu	
	125	
	ACAGGAGGGG CCGGATCTTT CTCCGATAAA ACCGTCGCCC TACAGACCCA GCTGTCCCCA	656
	CGCCTCTGTC TTTTGGGTCA AGTCTTAATC CCTGCACCTG AGTTGGTCCT CCCTCTGCAC	716
30	CCCCACCACC TCCTGCCCCG CTGGCAACTG GAAAGAAGGA GTTGGCCTGA TTTTAACCTT	776
	TTGCCGCTCC GGGGAACAGC ACAATCCTGG GCAGCCAGTG GCTCTTGTAG AGAAAACTTA	836
	GGATACCTCT CTCACCTTCT GTTTCTTGCC GTCCACCCCG GGCCATGCCA GTGTGTCTCTC	896
	TGGGTCCCCCT CCAAAAATCT GGTCATTCAA GGATCCCCCTC CCAAGGCTAT GCTTTTCTAT	956
	AACTTTTAAA TAAACCTTGG GGGGTGAATG GAATAAAAAA AAAAAAAAAA AAAAAA	1012
40		
	(2) INFORMATION FOR SEQ ID NO:4:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 150 amino acids	
	(B) TYPE: amino acid	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
	Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala	
	-23 -20 -15 -10	
	Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu	
	-5 1 5	

B'
Lnx.

Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
 10 15 20 25
 5 Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
 30 35 40
 Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
 45 50 55
 10 Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
 60 65 70
 Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His
 75 80 85
 15 Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys
 90 95 100 105
 20 Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile
 110 115 120
 Ser Ala Asn Ser Gly Leu
 125

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..288

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 79..288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG TGC TGT ACC AAG AGT TTG CTC CTG GCT GCT TTG ATG TCA GTG CTG 48
 Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
 50 -26 -25 -20 -15
 CTA CTC CAC CTC TGC GGC GAA TCA GAA GCA GCA AGC AAC TTT GAC TGC 96
 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
 55 -10 -5 1 5
 TGT CTT GGA TAC ACA GAC CGT ATT CTT CAT CCT AAA TTT ATT GTG GGC 144
 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
 10 15 20

B'
 cont.

5 TTC ACA CGG CAG CTG GCC AAT GAA GGC TGT GAC ATC AAT GCT ATC ATC 192
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35
 TTT CAC ACA AAG AAA AAG TTG TCT GTG TGC GCA AAT CCA AAA CAG ACT 240
 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
 40 45 50
 10 TGG GTG AAA TAT ATT GTG CGT CTC CTC AGT AAA AAA GTC AAG AAC ATG 288
 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
 55 60 65 70
 15 TAAAAACTGT GGCTTTTCTG GAATGGAATT GGACATAGCC CAAGAACAGA AAGAACCTTG 348
 CTGGGGTTGG AGGTTTCACT TGCACATCAT GGAGGGTTTA GTGCTTATCT AATTTGTGCC 408
 TCACTGGACT TGTCCAATTA ATGAAGTTGA TTCATATTGC ATCATAGTTT GCTTTGTTTA 468
 20 AGCATCACAT TAAAGTTAAA CTGTATTTTA TGTTATTTAT AGCTGTAGGT TTTCTGTGTT 528
 TAGCTATTTA ATACTAATTT TCCATAAGCT ATTTTGGTTT AGTGCAAAGT ATAAAATTAT 588
 ATTTGGGGGG GAATAAGATT ATATGGACTT TTTTGCAAGC AACAAGCTAT TTTTAAAAA 648
 25 AAATATTTA ACATTCTTTT GTTTATATTG TTTTGTCTCC TAAATTGTTG TAATTGCATT 708
 ATAAAAATAAG AAAAATATTA ATAAGACAAA TATTGAAAAT AAAGAAACAA AAAGTTAAAA 768
 30 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 801

(2) INFORMATION FOR SEQ ID NO:6:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

45 Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
 -26 -25 -20 -15
 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
 -10 -5 1 5
 50 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
 10 15 20
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35
 55 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
 40 45 50

B' cont.

Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
 55 60 65 70

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 699 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 142..435

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCACGAGCG GCACGAGCAT CACTCACACC TTGCATTTCA CCCCTGCATC CCAGTCGCCC 60
 25 TGCAGCCTCA CACAGATCCT GCACACACCC AGACAGCTGG CGCTCACACA TTCACCGTTG 120
 GCCTGCCTCT GTTCACCCTC C ATG GCC CTG CTA CTG GCC CTC AGC CTG CTG 171
 Met Ala Leu Leu Leu Ala Leu Ser Leu Leu
 1 5 10
 30 GTT CTC TGG ACT TCC CCA GCC CCA ACT CTG AGT GGC ACC AAT GAT GCT 219
 Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala
 15 20 25
 35 GAA GAC TGC TGC CTG TCT GTG ACC CAG AAA CCC ATC CCT GGG TAC ATC 267
 Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile
 30 35 40
 40 GTG AGG AAC TTC CAC TAC CTT CTC ATC AAG GAT GGC TGC AGG GTG CCT 315
 Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg Val Pro
 45 50 55
 GCT GTA GTG TTC ACC ACA CTG AGG GGC CGC CAG CTC TGT GCA CCC CCA 363
 Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro
 45 60 65 70
 GAC CAG CCC TGG GTA GAA CGC ATC ATC CAG AGA CTG CAG AGG ACC TCA 411
 Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser
 75 80 85 90
 50 GCC AAG ATG AAG CGC CGC AGC AGT TAACCTATGA CCGTGCAGAG GGAGCCCGGA 465
 Ala Lys Met Lys Arg Arg Ser Ser
 95
 55 GTCCGAGTCA AGCATTTGTGA ATTATTACCT AACCTGGGGA ACCGAGGACC AGAAGGAAGG 525
 ACCAGGCTTC CAGCTCCTCT GCACCAGACC TGACCAGCCA GGACAGGGCC TGGGGTGTGT 585

B'
 cont.

GTGAGTGTGA GTGTGAGCGA GAGGGTGAGT GTGGTCTAGA GTAAAGCTGC TCCACCCCCA 645

GATTGCAATG CTACCAATAA AGCCGCCTGG TGT'TTACAAC TAAAAAAAAA AAAA 699

5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
1 5 10 15

20

Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser
20 25 30

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
35 40 45

25

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
50 55 60

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
65 70 75 80

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Arg Arg
85 90 95

35

Ser Ser

(2) INFORMATION FOR SEQ ID NO:9:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1119 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

50

(A) NAME/KEY: CDS

(B) LOCATION: 1..1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

55

ATG TTT TCG ACT CCA GTG AAG ATT ATT TTG TGT CAG TCA ATA CTT CAT
Met Phe Ser Thr Pro Val Lys Ile Ile Leu Cys Gln Ser Ile Leu His
1 5 10 15

48

	ATT	ACT	CAG	TTG	ATT	CTG	AGA	TGT	TAC	TGT	GCT	CCT	TGC	AGG	AGG	TCA	96
	Ile	Thr	Gln	Leu	Ile	Leu	Arg	Cys	Tyr	Cys	Ala	Pro	Cys	Arg	Arg	Ser	
				20					25					30			
5	GGC	AGT	TCT	CCA	GGC	TAT	TTG	TAC	CGA	ATT	GCC	TAC	TCC	TTG	ATC	TGT	144
	Gly	Ser	Ser	Pro	Gly	Tyr	Leu	Tyr	Arg	Ile	Ala	Tyr	Ser	Leu	Ile	Cys	
			35				40						45				
10	GTT	CTT	GGC	CTC	CTG	GGG	AAT	ATT	CTG	GTG	GTG	ATC	ACC	TTT	GCT	TTT	192
	Val	Leu	Gly	Leu	Leu	Gly	Asn	Ile	Leu	Val	Val	Ile	Thr	Phe	Ala	Phe	
		50					55					60					
15	TAT	AAG	AAG	GCC	AGG	TCT	ATG	ACA	GAC	GTC	TAT	CTC	TTG	AAC	ATG	GCC	240
	Tyr	Lys	Lys	Ala	Arg	Ser	Met	Thr	Asp	Val	Tyr	Leu	Leu	Asn	Met	Ala	
	65					70				75					80		
20	ATT	GCA	GAC	ATC	CTC	TTT	GTT	CTT	ACT	CTC	CCA	TTC	TGG	GCA	GTG	AGT	288
	Ile	Ala	Asp	Ile	Leu	Phe	Val	Leu	Thr	Leu	Pro	Phe	Trp	Ala	Val	Ser	
				85					90						95		
25	CAT	GCC	ACT	GGT	GCG	TGG	GTT	TTC	AGC	AAT	GCC	ACG	TGC	AAG	TTG	CTA	336
	His	Ala	Thr	Gly	Ala	Trp	Val	Phe	Ser	Asn	Ala	Thr	Cys	Lys	Leu	Leu	
				100					105					110			
30	AAA	GGC	ATC	TAT	GCC	ATC	AAC	TTT	AAC	TGC	GGG	ATG	CTG	CTC	CTG	ACT	384
	Lys	Gly	Ile	Tyr	Ala	Ile	Asn	Phe	Asn	Cys	Gly	Met	Leu	Leu	Leu	Thr	
			115				120						125				
35	TGC	ATT	AGC	ATG	GAC	CGG	TAC	ATC	GCC	ATT	GTA	CAG	GCG	ACT	AAG	TCA	432
	Cys	Ile	Ser	Met	Asp	Arg	Tyr	Ile	Ala	Ile	Val	Gln	Ala	Thr	Lys	Ser	
		130					135					140					
40	TTC	CGG	CTC	CGA	TCC	AGA	ACA	CTA	CCG	CGC	AGC	AAA	ATC	ATC	TGC	CTT	480
	Phe	Arg	Leu	Arg	Ser	Arg	Thr	Leu	Pro	Arg	Ser	Lys	Ile	Ile	Cys	Leu	
		145				150					155					160	
45	GTT	GTG	TGG	GGG	CTG	TCA	GTC	ATC	ATC	TCC	AGC	TCA	ACT	TTT	GTC	TTC	528
	Val	Val	Trp	Gly	Leu	Ser	Val	Ile	Ile	Ser	Ser	Ser	Thr	Phe	Val	Phe	
				165					170						175		
50	AAC	CAA	AAA	TAC	AAC	ACC	CAA	GGC	AGC	GAT	GTC	TGT	GAA	CCC	AAG	TAC	576
	Asn	Gln	Lys	Tyr	Asn	Thr	Gln	Gly	Ser	Asp	Val	Cys	Glu	Pro	Lys	Tyr	
				180					185					190			
55	CAA	ACT	GTC	TCG	GAG	CCC	ATC	AGG	TGG	AAG	CTG	CTG	ATG	TTG	GGG	CTT	624
	Gln	Thr	Val	Ser	Glu	Pro	Ile	Arg	Trp	Lys	Leu	Leu	Met	Leu	Gly	Leu	
			195				200						205				
60	GAG	CTA	CTC	TTT	GGT	TTC	TTT	ATC	CCT	TTG	ATG	TTC	ATG	ATA	TTT	TGT	672
	Glu	Leu	Leu	Phe	Gly	Phe	Phe	Ile	Pro	Leu	Met	Phe	Met	Ile	Phe	Cys	
		210					215					220					
65	TAC	ACG	TTC	ATT	GTC	AAA	ACC	TTG	GTG	CAA	GCT	CAG	AAT	TCT	AAA	AGG	720
	Tyr	Thr	Phe	Ile	Val	Lys	Thr	Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg	
	225					230					235					240	

B'
cont.

5	CAC AAA GCC ATC CGT GTA ATC ATA GCT GTG GTG CTT GTG TTT CTG GCT His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala 245 250 255	768
10	TGT CAG ATT CCT CAT AAC ATG GTC CTG CTT GTG ACG GCT GCT AAT TTG Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu 260 265 270	816
15	GGT AAA ATG AAC CGA TCC TGC CAG AGC GAA AAG CTA ATT GGC TAT ACG Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr 275 280 285	864
20	AAA ACT GTC ACA GAA GTC CTG GCT TTC CTG CAC TGC TGC CTG AAC CCT Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro 290 295 300	912
25	GTG CTC TAC GCT TTT ATT GGG CAG AAG TTC AGA AAC TAC TTT CTG AAG Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys 305 310 315 320	960
30	ATC TTG AAG GAC CTG TGG TGT GTG AGA AGG AAG TAC AAG TCC TCA GGC Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly 325 330 335	1008
35	TTC TCC TGT GCC GGG AGG TAC TCA GAA AAC ATT TCT CGG CAG ACC AGT Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser 340 345 350	1056
40	GAG ACC GCA GAT AAC GAC AAT GCG TCG TCC TTC ACT ATG TGATAGAAAG Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met 355 360 365	1105
45	CTGAGTCTCC CTAA	1119

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

50	Met Phe Ser Thr Pro Val Lys Ile Ile Leu Cys Gln Ser Ile Leu His 1 5 10 15
55	Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser 20 25 30
60	Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys 35 40 45
65	Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe 50 55 60

Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
 65 70 75 80
 5 Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser
 85 90 95
 His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu
 100 105 110
 10 Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr
 115 120 125
 Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
 130 135 140
 15 Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu
 145 150 155 160
 20 Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe
 165 170 175
 Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr
 180 185 190
 25 Gln Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu
 195 200 205
 Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Met Phe Met Ile Phe Cys
 210 215 220
 Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg
 225 230 235 240
 35 His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala
 245 250 255
 Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu
 260 265 270
 40 Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr
 275 280 285
 Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro
 290 295 300
 Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys
 305 310 315 320
 50 Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly
 325 330 335
 Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser
 340 345 350
 55 Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met
 355 360 365

B'
 cont.

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 1547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 49..1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGGAAGCTG CTTCTGGGGG TGAGCAAAC TTTTAAATG CAGAAATT ATG ATC TAC																57
Met Ile Tyr																
1																
ACC	CGT	TTC	TTA	AAA	GGC	AGT	CTG	AAG	ATG	GCC	AAT	TAC	ACG	CTG	GCA	105
Thr	Arg	Phe	Leu	Lys	Gly	Ser	Leu	Lys	Met	Ala	Asn	Tyr	Thr	Leu	Ala	
5					10					15						
CCA	GAG	GAT	GAA	TAT	GAT	GTC	CTC	ATA	GAA	GGT	GAA	CTG	GAG	AGC	GAT	153
Pro	Glu	Asp	Glu	Tyr	Asp	Val	Leu	Ile	Glu	Gly	Glu	Leu	Glu	Ser	Asp	
20					25					30						
GAG	GCA	GAG	CAA	TGT	GAC	AAG	TAT	GAC	GCC	CAG	GCA	CTC	TCA	GCC	CAG	201
Glu	Ala	Glu	Gln	Cys	Asp	Lys	Tyr	Asp	Ala	Gln	Ala	Leu	Ser	Ala	Gln	
40					45					50						
CTG	GTG	CCA	TCA	CTC	TGC	TCT	GCT	GTG	TTT	GTG	ATC	GGT	GTC	CTG	GAC	249
Leu	Val	Pro	Ser	Leu	Cys	Ser	Ala	Val	Phe	Val	Ile	Gly	Val	Leu	Asp	
55					60					65						
AAT	CTC	CTG	GTT	GTG	CTT	ATC	CTG	GTA	AAA	TAT	AAA	GGA	CTC	AAA	CGC	297
Asn	Leu	Leu	Val	Val	Leu	Ile	Leu	Val	Lys	Tyr	Lys	Gly	Leu	Lys	Arg	
70					75					80						
GTG	GAA	AAT	ATC	TAT	CTT	CTA	AAC	TTG	GCA	GTT	TCT	AAC	TTG	TGT	TTC	345
Val	Glu	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Val	Ser	Asn	Leu	Cys	Phe	
85					90					95						
TTG	CTT	ACC	CTG	CCC	TTC	TGG	GCT	CAT	GCT	GGG	GGC	GAT	CCC	ATG	TGT	393
Leu	Leu	Thr	Leu	Pro	Phe	Trp	Ala	His	Ala	Gly	Gly	Asp	Pro	Met	Cys	
100					105					110						
AAA	ATT	CTC	ATT	GGA	CTG	TAC	TTC	GTG	GGC	CTG	TAC	AGT	GAG	ACA	TTT	441
Lys	Ile	Leu	Ile	Gly	Leu	Tyr	Phe	Val	Gly	Leu	Tyr	Ser	Glu	Thr	Phe	
120					125					130						
TTC	AAT	TGC	CTT	CTG	ACT	GTG	CAA	AGG	TAC	CTA	GTG	TTT	TTG	CAC	AAG	489
Phe	Asn	Cys	Leu	Leu	Thr	Val	Gln	Arg	Tyr	Leu	Val	Phe	Leu	His	Lys	
135					140					145						

	GGC AAC TTT TTC TCA GCC AGG AGG AGG GTG CCC TGT GGC ATC ATT ACA	537
	Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly Ile Ile Thr	
	150 155 160	
5	AGT GTC CTG GCA TGG GTA ACA GCC ATT CTG GCC ACT TTG CCT GAA TTC	585
	Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu Pro Glu Phe	
	165 170 175	
10	GTG GTT TAT AAA CCT CAG ATG GAA GAC CAG AAA TAC AAG TGT GCA TTT	633
	Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys Cys Ala Phe	
	180 185 190 195	
15	AGC AGA ACT CCC TTC CTG CCA GCT GAT GAG ACA TTC TGG AAG CAT TTT	681
	Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp Lys His Phe	
	200 205 210	
20	CTG ACT TTA AAA ATG AAC ATT TCG GTT CTT GTC CTC CCC CTA TTT ATT	729
	Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro Leu Phe Ile	
	215 220 225	
25	TTT ACA TTT CTC TAT GTG CAA ATG AGA AAA ACA CTA AGG TTC AGG GAG	777
	Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg Phe Arg Glu	
	230 235 240	
30	CAG AGG TAT AGC CTT TTC AAG CTT GTT TTT GCC GTA ATG GTA GTC TTC	825
	Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met Val Val Phe	
	245 250 255	
35	CTT CTG ATG TGG GCG CCC TAC AAT ATT GCA TTT TTC CTG TCC ACT TTC	873
	Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu Ser Thr Phe	
	260 265 270 275	
40	AAA GAA CAC TTC TCC CTG AGT GAC TGC AAG AGC AGC TAC AAT CTG GAC	921
	Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr Asn Leu Asp	
	280 285 290	
45	AAA AGT GTT CAC ATC ACT AAA CTC ATC GCC ACC ACC CAC TGC TGC ATC	969
	Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His Cys Cys Ile	
	295 300 305	
50	AAC CCT CTC CTG TAT GCG TTT CTT GAT GGG ACA TTT AGC AAA TAC CTC	1017
	Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu	
	310 315 320	
55	TGC CGC TGT TTC CAT CTG CGT AGT AAC ACC CCA CTT CAA CCC AGG GGG	1065
	Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly	
	325 330 335	
60	CAG TCT GCA CAA GGC ACA TCG AGG GAA GAA CCT GAC CAT TCC ACC GAA	1113
	Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu	
	340 345 350 355	
65	GTG TAAACTAGCA TCCACCAAAT GCAAGAAGAA TAAACATGGA TTTTCATCTT	1166
	Val	
70	TCTGCATTAT TTCATGTAAA TTTTCTACAC ATTTGTATAC AAAATCGGAT ACAGGAAGAA	1226

AAGGGAGAGG TGAGCTAACA TTTGCTAAGC ACTGAATTTG TCTCAGGCAC CGTGCAAGGC 1286
 TCTTTACAAA CGTGAGCTCC TTCGCCTCCT ACCACTTGTC CATAGTGTGG ATAGGACTAG 1346
 5 TCTCATTTCT CTGAGAAGAA AACTAAGGCG CGGAAATTTG TCTAAGATCA CATAACTAGG 1406
 AAGTGGCAGA ACTGATTCTC CAGCCCTGGT AGCATTTGCT CAGAGCCTAC GCTTGGTCCA 1466
 GAACATCAAA CTCCAAACCC TGGGGACAAA CGACATGAAA TAAATGTATT TTAAACATA 1526
 10 TAAAAAAAAA AAAAAAAAAA A 1547

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

25 Met Ile Tyr Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr
 1 5 10 15
 Thr Leu Ala Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu
 20 25 30
 30 Glu Ser Asp Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu
 35 40 45
 Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly
 35 50 55 60
 Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly
 65 70 75 80
 40 Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn
 85 90 95
 Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp
 100 105 110
 45 Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser
 115 120 125
 Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe
 50 130 135 140
 Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly
 145 150 155 160
 55 Ile Ile Thr Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu
 165 170 175

B'
 cont.

Pro Glu Phe Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys
 180 185 190
 5 Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp
 195 200 205
 Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro
 210 215 220
 10 Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg
 225 230 235 240
 Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met
 245 250 255
 15 Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu
 260 265 270
 Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr
 275 280 285
 Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His
 290 295 300
 25 Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser
 305 310 315 320
 Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln
 325 330 335
 B' unx. 30 Pro Arg Gly Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His
 340 345 350
 Ser Thr Glu Val
 35 355

(2) INFORMATION FOR SEQ ID NO:13:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
 1 5 10 15
 55 Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
 20 25 30

Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
 35 40 45
 5 Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
 50 55 60
 10 Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80
 10 Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
 85 90 95
 15 Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
 100 105 110
 Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
 115 120 125
 20 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
 130 135 140
 25 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu
 145 150 155 160
 25 Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
 165 170 175
 30 Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
 180 185 190
 Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
 195 200 205
 35 Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
 210 215 220
 40 Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
 225 230 235 240
 Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn
 245 250 255
 45 Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu
 260 265 270
 Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val
 275 280 285
 50 Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val
 290 295 300
 55 Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val
 305 310 315 320
 Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu
 325 330 335

B'
 cont.

Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu Ser
 340 345 350

Ala Gly Phe
 355

5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

20 Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
 1 5 10 15

Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
 20 25 30

25 His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
 35 40 45

Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
 50 55 60

30 Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
 65 70 75 80

35 Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
 85 90 95

Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
 100 105 110

40 Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
 115 120 125

Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
 130 135 140

45 Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
 145 150 155 160

50 Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
 165 170 175

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 180 185 190

55 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 195 200 205

B'
 cont.

5 Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 210 215 220
 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 225 230 235 240
 10 Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 245 250 255
 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270
 15 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
 275 280 285
 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300
 20 Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
 305 310 315 320
 Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
 325 330 335
 25 Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
 340 345 350
 30 Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
 355 360 365
 Gln Asp Lys Glu Gly Ala
 370

35 (2) INFORMATION FOR SEQ ID NO:15:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr
 1 5 10 15
 50 Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
 20 25 30
 Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
 35 40 45
 55 Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
 50 55 60

81
cont.

5 Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80
 Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
 85 90 95
 His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
 100 105 110
 10 Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
 115 120 125
 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
 130 135 140
 15 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
 145 150 155 160
 20 Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
 165 170 175
 Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
 180 185 190
 25 Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
 195 200 205
 Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
 210 215 220
 30 Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
 225 230 235 240
 Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
 245 250 255
 Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
 260 265 270
 40 Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
 275 280 285
 Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
 290 295 300
 45 Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
 305 310 315 320
 Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
 325 330 335
 Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
 340 345 350
 55 Ile Val Phe
 355

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
 1 5 10 15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
 20 25 30

Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
 35 40 45

Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
 50 55 60

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
 65 70 75 80

Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
 85 90 95

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
 100 105 110

Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
 115 120 125

Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
 130 135 140

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
 145 150 155 160

Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
 165 170 175

Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
 180 185 190

Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
 195 200 205

Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
 210 215 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
 225 230 235 240

Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
 245 250 255

B'
 cont.

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
 260 265 270
 5 Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
 275 280 285
 Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
 290 295 300
 10 Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
 305 310 315 320
 Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
 325 330 335
 15 Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
 340 345 350
 Asp His Asp Leu His Asp Ala Leu
 355 360
 20

(2) INFORMATION FOR SEQ ID NO:17:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: cDNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

35 GTAATGATCA GTCAACGGGG GAC

23

(2) INFORMATION FOR SEQ ID NO:18:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: cDNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

50 CCAGCAAGCT TGCAACCTTA ACCA

24

(2) INFORMATION FOR SEQ ID NO:19:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 Asp Tyr Lys Asp Asp Asp Asp Lys Leu
1 5

B'
concl.